

SEQUENCE LISTING

<110> Gentide Biopharmaceuticals, Inc.
Russell, Stuart

<120> METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENCES AS
DIRECT FUSIONS OR WITH LINKERS

<130> GNT-00101.P.1-US

<150> US 60/396,466

<151> 2002-07-16

<160> 86

<170> PatentIn version 3.0

<210> 1

<211> 573

<212> DNA

<213> Homo sapiens

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 35 40 45
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
 50 55 60
 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
 65 70 75 80
 Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
 85 90 95
 Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
 100 105 110
 Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
 115 120 125
 Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
 130 135 140
 Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
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 Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
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 Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
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35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

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130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
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Thr Val Ala Gln Ala
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Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	35	40	45	
Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	50	55	60	
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Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	115	120	125	
Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	130	135	140	
Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	145	150	155	160
Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	165	170	175	
Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	180	185	190	
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Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
180 185

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Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
 35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
 50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
 65 70 75 80

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
 85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
 100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
 115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
 130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
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 165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
 180 185 190

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Ser Cys Gly Phe Lys Lys Lys

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5

<210> 26

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120

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 tccaacaggg aggaaacaca acagaaatcc aacctagagc tgctccgcat ctccctgctg 840
 ctcattcagt cgtggctgga gcccgctgag ttcttcagga gtgtcttcgc caacagcctg 900
 gtgtacggcg cctctgacag caacgtctat gacctcctaa aggacctaga ggaaggcatc 960
 caaacgctga tggggaggct ggaagatggc agcccccgga ctgggcagat cttcaagcag 1020
 acctacagca agttcgacac aaactcacac aacgatgacg cactactcaa gaactacggg 1080
 ctgctctact gcttcaggaa ggacatggac aaggctgaga cattcctgcg catcgtgcag 1140
 tgccgctctg tggagggatc c 1161

<210> 27

<211> 382

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<400> 27

Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
 1 5 10 15

Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
 20 25 30

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
 35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
 50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
 65 70 75 80

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
 85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
 100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
 115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
 130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
 145 150 155 160

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
 165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser
 180 185 190

Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala
 195 200 205

Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
 210 215 220

Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu
 225 230 235 240

Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro
 245 250 255

Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg
 260 265 270

Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu
 275 280 285

Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn
 290 295 300

Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met
 305 310 315 320

Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln
 325 330 335

Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu
 340 345 350

Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val
355 360 365

Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
370 375 380

<210> 28

<211> 1152

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc_feature

<222> (574)..(1146)

<223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 28

tgatcatgtg gcttcttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60

cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 120

atccc aaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca 180

gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg 240

ctccgcatct cctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 300

gtcttcgcca acagcctggg gtacggcgcc tctgacagca acgtctatga cctcctaaag 360

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420

gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480

ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540

ttcctgcgca tcgtgcagtg ccgctctgtg gagggatcat gtggcttctt cccaaccatt 600

cccttatcca ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc 660

tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc 720

ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg 780

gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct gctcatccag 840

tcgtggctgg agcccgtgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc 900

gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaacgctg 960

atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca gacctacagc 1020

aagtctgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac 1080

tgcttcagga aggacatgga caaggtcgag acattcctgc gcatcgtgca gtgccgctct 1140

gtggagggat cc 1152

<210> 29

<211> 382

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC_FEATURE

<222> (191)..(381)

<223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 29

Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
1 5 10 15

Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
20 25 30

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr
50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
65 70 75 80

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe
85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser
100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys
130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu
145 150 155 160

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys
165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser

180										185					190									
Cys	Gly	Phe	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala									
195										200					205									
Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln									
210			215					220																
Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu									
225		230					235					240												
Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro									
245					250					255														
Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg									
260			265					270																
Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu									
275			280					285																
Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn									
290		295					300																	
Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met									
305		310					315					320												
Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln									
325				330					335															
Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu									
340			345					350																
Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val									
355		360					365																	
Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly											
370			375					380																

<210> 30
 <211> 606
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 30	
catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac	60
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag	120
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt	180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac	240
tcctgtctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc	300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggatcc gaattccatt gatcatgtgg cttctagtag	600
gtcgac	606

<210> 31
 <211> 1737
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<220>
 <221> misc_feature
 <222> (1138)..(1710)
 <223> sequence is repeated N-1 times, where N is a positive whole number

<400> 31	
catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgccccat	60
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag	120
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt	180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac	240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc	300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggatca tgtggcttct tcccaaccat tcccttatcc	600
aggctttttg acaacgctat gctccgcgcc catcgtctgc accagctggc ctttgacacc	660
taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac	720
ccccagacct cctctgttt ctcagagtct attccgacac cctccaacag ggaggaaaca	780
caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg	840

gagcccggtgc agttcctcag gagtgtcttc gccaacagcc tgggtgtacgg cgcctctgac 900
 agcaacgtct atgacctcct aaaggacctt gaggaaggca tccaaacgct gatggggagg 960
 ctggaagatg gcagcccccg gactgggcag atcttcaagc agacctacag caagtctgac 1020
 acaaactcac acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg 1080
 aaggacatgg acaaggtcga gacattcctg cgcacgtgc agtgccgctc tgtggaggga 1140
 tcatgtgggt tcttcccaac cattccctta tccaggcttt ttgacaacgc tatgctccgc 1200
 gcccatcgtc tgcaccagct ggcctttgac acctaccagg agtttgaaga agcctatata 1260
 ccaaaggaaac agaagtattc attcctgcag aacccccaga cctccctctg tttctcagag 1320
 tctattccga caccctccaa cagggaggaa acacaacaga aatccaacct agagctgctc 1380
 cgcactctcc tgcgtctcat ccagtcgtgg ctggagcccg tgcagttcct caggagtgtc 1440
 ttgcgaaca gcctgggtga cggcgctct gacagcaacg tctatgacct cctaaaggac 1500
 ctagaggaag gcatccaaac gctgatgggg aggctggaag atggcagccc ccggactggg 1560
 cagatcttca agcagacctt cagcaagttc gacacaaact cacacaacga tgacgcacta 1620
 ctcaagaact acggggtgct ctactgcttc aggaaggaca tggacaaggt cgagacattc 1680
 ctgcgcacgc tgcagtggcg ctctgtggag ggatcatgtg gcttctagta ggtcgac 1737

<210> 32
 <211> 574
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic sequence

<220>
 <221> MISC_FEATURE
 <222> (379)..(569)
 <223> sequence is repeated N-1 times, where N is a positive whole number

<220>
 <221> mat_peptide
 <222> (1)..()

<400> 32

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190
 Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
 195 200 205
 Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
 210 215 220
 Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
 225 230 235 240
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
 245 250 255
 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
 260 265 270
 Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
 275 280 285
 Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
 290 295 300
 Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
 305 310 315 320
 Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
 325 330 335

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
 340 345 350
 Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
 355 360 365
 Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Phe
 370 375 380
 Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala
 385 390 395 400
 His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu
 405 410 415
 Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln
 420 425 430
 Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu
 435 440 445
 Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu
 450 455 460
 Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe
 465 470 475 480
 Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu
 485 490 495
 Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu
 500 505 510
 Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys
 515 520 525
 Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
 530 535 540
 Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu
 545 550 555 560
 Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 565 570

<210> 33

<211> 55

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 33

taccatgatga catgatcatg tggcttcggg ttcccaacca ttcccttata caggc

<210> 34
<211> 591
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 34
catatgacat gatcatgtgg cttcggtttc ccaaccattc ccttatccag gctttttgac 60
aacgctatgc tccgcgcccc tcgtctgcac cagctggcct ttgacaccta ccaggagttt 120
gaagaagcct atatcccaaa ggaacagaag tattcattcc tgcagaaccc ccagacctcc 180
ctctgtttct cagagtctat tccgacaccc tccaacaggg aggaaacaca acagaaatcc 240
aacctagagc tgctccgcat ctccctgctg ctcatccagt cgtggctgga gcccgctgcag 300
ttcctcagga gtgtcttcgc caacagcctg gtgtacggcg cctctgacag caacgtctat 360
gacctcctaa aggacctaga ggaaggcatc caaacgctga tggggaggct ggaagatggc 420
agcccccgga ctgggcagat cttcaagcag acctacagca agttcgacac aaactcacac 480
aacgatgacg cactactcaa gaactacggg ctgctctact gcttcaggaa ggacatggac 540
aaggtcgaga cattcctgcg catcgtgcag tgccgctctg tggagggatc c 591

<210> 35
<211> 192
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 35

Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp
1 5 10 15

Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr
20 25 30

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser
35 40 45

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro
50 55 60

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu
65 70 75 80

Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp
100 105 110

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr
115 120 125

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe
130 135 140

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala
145 150 155 160

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp
165 170 175

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
180 185 190

<210> 36

<211> 1158

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc_feature

<222> (577)..(1152)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 36

tgatcatgtg gcttcggttt cccaaccatt cccttatcca ggctttttga caacgctatg 60

ctccgcgccc atcgtctgca ccagctggcc tttgacacct accaggagtt tgaagaagcc 120

tatatcccaa aggaacagaa gtattcattc ctgcagaacc ccagacctc cctctgtttc 180

tcagagtcta ttccgacacc ctccaacagg gaggaacac aacagaaatc caacctagag 240

ctgctccgca tctccctgct gctcatccag tcgtggctgg agcccgtgca gttcctcagg 300

agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca gcaacgtcta tgacctccta 360

aaggacctag aggaaggcat ccaaacgctg atggggaggc tggaagatgg cagcccccg 420

actgggcaga tcttcaagca gacctacagc aagttcgaca caaactcaca caacgatgac 480

gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggtcgag 540

acattcctgc gcacgtgca gtgccgtct gtggagggat catgtggctt cggtttccca 600

accattcct tatccaggct ttttgacaac gctatgctcc gcgcccatcg tctgcaccag 660

ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat 720
 tcattcctgc agaaccacca gacctccctc tgtttctcag agtctattcc gacaccctcc 780
 aacagggagg aaacacaaca gaaatccaac ctagagctgc tccgcatctc cctgctgctc 840
 atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcttcgcca cagcctgggtg 900
 tacggcgcct ctgacagcaa cgtctatgac ctctaaagg acctagagga aggcattccaa 960
 acgctgatgg ggaggctgga agatggcagc ccccgactg ggcatatctt caagcagacc 1020
 tacagcaagt tcgacacaaa ctacacaaac gatgacgcac tactcaagaa ctacgggctg 1080
 ctctactgct tcaggaagga catggacaag gtcgagacat tcttgcgcat cgtgcagtgc 1140
 cgctctgtgg agggatcc 1158

<210> 37
 <211> 384
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic sequence

<220>
 <221> MISC_FEATURE
 <222> (192)..(383)
 <223> sequence is repeated N-1 times, where N is a positive whole number

<400> 37

Ser	Cys	Gly	Phe	Gly	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp
1				5					10					15	
Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr
			20					25					30		
Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser
	35						40					45			
Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro
	50					55					60				
Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu
65					70					75				80	
Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln
				85					90					95	
Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp
			100					105						110	

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr
115 120 125

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe
130 135 140

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala
145 150 155 160

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp
165 170 175

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
180 185 190

Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp
195 200 205

Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr
210 215 220

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser
225 230 235 240

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro
245 250 255

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu
260 265 270

Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln
275 280 285

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp
290 295 300

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr
305 310 315 320

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe
325 330 335

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala
340 345 350

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp
355 360 365

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly
370 375 380

<210> 38
<211> 1743
<212> DNA
<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc_feature

<222> (1141)..(1716)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 38

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catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac      60
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag    120
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt    180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcctc    240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc     300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag    360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc    420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag    480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc    540
atcgtgcagt gccgctctgt ggagggatca tgtggcttcg gtttcccaac cattccctta    600
tccaggcttt ttgacaacgc tatgctccgc gcccatcgtc tgcaccagct ggcctttgac    660
acctaccagg agtttgaaga agcctatatc ccaaaggaa acagaatttc attcctgcag    720
aacccccaga cctcctctg tttctcagag tctattccga caccctcaa caggaggagaa    780
acacaacaga aatccaacct agagctgctc cgcctctccc tgctgctcat ccagtcgtgg    840
ctggagcccc tgcagttcct caggagtgtc ttgcgcaaca gcttgggtgta cggcgctctc    900
gacagcaacg tctatgacct cctaaaggac ctagaggaag gcatccaaac gctgatgggg    960
aggctggaag atggcagccc ccggactggg cagatcttca agcagacctc cagcaagttc   1020
gacacaaact cacacaacga tgacgcacta ctcaagaact acgggctgct ctactgcttc   1080
aggaaggaca tggacaaggt cgagacattc ctgcgcctcg tgcagtgccg ctctgtggag   1140
ggatcatgtg gcttcggttt cccaaccatt cccttatcca ggctttttga caacgctatg   1200
ctccgcgccc atcgtctgca ccagctggcc ttgacacct accaggagtt tgaagaagcc   1260
tatatcccaa aggaacagaa gtattcattc ctgcagaacc ccagacctc cctctgtttc   1320
tcagagtcta ttccgacacc ctccaacagg gaggaacac aacagaaatc caacctagag   1380
```

```

ctgctccgca tctccctgct gctcatccag tegtggctgg agcccgtag gttcctcagg 1440
agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca gcaacgtcta tgacctccta 1500
aaggacctag aggaaggcat ccaaacgctg atggggaggc tggaagatgg cagcccccg 1560
actgggcaga tcttcaagca gacctacagc aagttcgaca caaactcaca caacgatgac 1620
gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggctcag 1680
acattcctgc gcatcgtgca gtgccgctct gtggagggat catgtggctt ctagtaggtc 1740
gac 1743

```

```

<210> 39
<211> 576
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<220>
<221> MISC_FEATURE
<222> (380)..(571)
<223> sequence is repeated N-1 times, where N is a positive whole numbe

```

```

<220>
<221> mat_peptide
<222> (1)..()

```

```

<400> 39

```

```

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1      5      10      15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
      20      25      30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
      35      40      45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
      50      55      60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65      70      75      80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
      85      90      95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
      100      105      110

```

Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg		
	115						120					125					
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr		
	130					135					140						
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn		
145					150				155						160		
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr		
				165					170					175			
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe		
			180					185					190				
Gly	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu		
		195					200					205					
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe		
	210					215					220						
Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn		
225					230					235					240		
Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn		
				245					250					255			
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser		
			260					265					270				
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser		
		275					280					285					
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr		
	290					295					300						
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg		
305					310					315					320		
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr		
				325					330					335			
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn		
			340					345					350				
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr		
		355					360					365					
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe		
		370				375					380						
Gly	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu		
385					390					395					400		
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe		
				405					410					415			

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 420 425 430

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 435 440 445

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 450 455 460

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 465 470 475 480

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 485 490 495

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 500 505 510

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 515 520 525

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 530 535 540

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 545 550 555 560

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 565 570 575

<210> 40
 <211> 39
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 40
 cgcggtcct catgagaagc cacagctgcc ctccacaga

39

<210> 41
 <211> 591
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 41
 catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccat

60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag

120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt

180

ccgacaccct ccaacagggg ggaacacaaa cagaaatcca acctagagct gctccgcac 240
 tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc 300
 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360
 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420
 ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag 480
 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540
 atcgtgcagt gccgtctgt ggagggcagc tgtggcttct catgaggatc c 591

<210> 42

<211> 193

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<400> 42

Met	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu
1				5					10					15	
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe
			20					25					30		
Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn
		35					40					45			
Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn
		50				55					60				
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser
65					70					75					80
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser
			85					90						95	
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
			100					105					110		
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg
		115				120						125			
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr
	130					135					140				
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn
145					150				155						160
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr
			165					170						175	

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

Ser

<210> 43
<211> 50
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 43
catgccatgg ggtggtggag gaagtttccc aaccattccc ttatccaggc 50

<210> 44
<211> 606
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 44
ccatgggggtg gtggaggaag ttccccaacc attcccttat ccaggctttt tgacaacgct 60
atgctccgcg cccatcgtct gcaaccagctg gcctttgaca cctaccagga gtttgaagaa 120
gcctatatcc caaaggaaca gaagtattca ttccctgcaga acccccagac ctccctctgt 180
ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240
gagctgctcc gcattccctt gctgctcatt cagtcgtggc tggagcccgt gcagttcctc 300
aggagtgtct tcgccaacag cctgggtgtac ggccgctctg acagcaacgt ctatgacctc 360
ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc 420
cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat 480
gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540
gagacattcc tgcgcacgtg gcagtgccgc tctgtggagg gcagctgtgg cttctcatga 600
ggatcc 606

<210> 45
<211> 198
<212> PRT
<213> Artificial

<220>

<223> synthetic sequence

<400> 45

Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
1 5 10 15

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
20 25 30

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
50 55 60

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln
115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile
130 135 140

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp
145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met
165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu
180 185 190

Gly Ser Cys Gly Phe Ser
195

<210> 46

<211> 603

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 46

ccatgggggtg gtggaggaag tttcccaacc attcccttat ccaggctttt tgacaacgct 60

atgctccgcg cccatcgctc gcaccagctg gcctttgaca cctaccagga gtttgaagaa 120

gcctatatcc caaaggaaca gaagtattca ttctctgcaga acccccagac ctccctctgt 180

ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240
 gagctgctcc gcattctcct gctgctcacc cagtcgtggc tggagcccgt gcagttcctc 300
 aggagtgtct tcgccaacag cctgggtgtac ggcgcctctg acagcaacgt ctatgacctc 360
 ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc 420
 cggactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat 480
 gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540
 gagacattcc tgcgcatcgt gcagtgccgc tctgtggagg gcagctgtgg cttctagggg 600
 tcc 603

<210> 47
 <211> 197
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 47

Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
 1 5 10 15
 Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
 20 25 30
 Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
 35 40 45
 Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
 50 55 60
 Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
 65 70 75 80
 Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
 85 90 95
 Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
 100 105 110
 Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln
 115 120 125
 Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile
 130 135 140
 Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp
 145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met
 165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu
 180 185 190

Gly Ser Cys Gly Phe
 195

<210> 48

<211> 1200

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc feature

<222> (595)..(1188)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 48

ccatggggtg gtggaggaag tttcccaacc attcccttat ccaggtttt tgacaacgct	60
atgctccgcg cccatcgtct gcaccagctg gcctttgaca cctaccagga gtttgaagaa	120
gcctatatcc caaaggaaca gaagtattca ttcctgcaga acccccagac ctccctctgt	180
ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta	240
gagctgctcc gcctctccct gctgctcatc cagtcgtggc tggagcccgt gcagttcctc	300
aggagtgtct tcgccaacag cctggtgtac ggcgcctctg acagcaacgt ctatgacctc	360
ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc	420
eggactgggc agatcttcaa gcagacctac agcaagtctg acacaaactc acacaacgat	480
gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc	540
gagacattcc tgcgcatcgt gcagtgccgc tctgtggagg gcagctgtgg cttctcatgg	600
gggtggtggag gaagtttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc	660
cgcgcccata gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat	720
atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca	780
gagtctattc cgacacctc caacaggag gaaacacaac agaaatccaa cctagagctg	840
ctccgcatct cctgctgct catccagtcg tggtggagc ccgtgcagtt cctcaggagt	900
gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag	960

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 1020
 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 1080
 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 1140
 ttctctgcga tcgtgcagtg ccgctctgtg gagggcagct gtggcttctc atgaggatcc 1200

<210> 49

<211> 396

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC FEATURE

<222> (198)..(395)

<223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 49

Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
 1 5 10 15

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp
 20 25 30

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr
 35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile
 50 55 60

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu
 65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val
 85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser
 100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln
 115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile
 130 135 140

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp
 145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met
165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu
180 185 190

Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile
195 200 205

Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu
210 215 220

His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile
225 230 235 240

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu
245 250 255

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln
260 265 270

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln
275 280 285

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser
290 295 300

Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp
305 310 315 320

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser
325 330 335

Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr
340 345 350

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr
355 360 365

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val
370 375 380

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser
385 390 395

<210> 50

<211> 1185

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 50

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccat 60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120

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gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180
ccgacaccct ccaacagggg ggaaacacaa cagaaatcca acctagagct gctccgcatc 240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc 300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gcccccgac tgggcagatc 420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540
atcgtgcagt gccgctctgt ggagggcagc tgtgggttct catgggggtg tggaggaagt 600
ttcccaacca ttcccttata caggcttttt gacaacgcta tgctccgcgc ccatcgtctg 660
caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 720
aagtattcat tctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca 780
ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg 840
ctgctcatcc agtcgtggct ggagcccgtg cagttcctca ggagtgtctt cgccaacagc 900
ctgggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc 960
atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag 1020
cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac 1080
gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacgtg 1140
cagtgccgct ctgtggaggg cagctgtggc ttctcatgag gatcc 1185

```

```

<210> 51
<211> 391
<212> PRT
<213> Artificial

```

```

<220>
<223> synthetic sequence

```

```

<220>
<221> mat_peptide
<222> (1)..()

```

```

<400> 51

```

```

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1           5           10          15
Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20          25          30

```

Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	35	40	45
Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	50	55	60
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	65	70	75
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	85	90	95
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	100	105	110
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	115	120	125
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	130	135	140
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	145	150	155
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	165	170	175
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	180	185	190
Ser	Trp	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	195	200	205
Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	210	215	220
Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	225	230	235
Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	245	250	255
Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	260	265	270
Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	275	280	285
Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	290	295	300
Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	305	310	315
Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	325	330	335

Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp
340 345 350

Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp
355 360 365

Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val
370 375 380

Glu Gly Ser Cys Gly Phe Ser
385 390

<210> 52

<211> 1779

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc_feature

<222> (1174)..(1767)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 52

catatgtttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180

ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240

tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540

atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catggggtgg tggaggaagt 600

ttcccaacca ttcccttatc caggcttttt gacaacgcta tgctccgcgc ccatcgtctg 660

caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 720

aagtattcat tctgcagaa ccccagacc tccctctgtt tctcagagtc tattccgaca 780

ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg 840

ctgctcatcc agtcgtggct ggagcccgct cagttcctca ggagtgtctt cgccaacagc 900
 ctgggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggg 960
 atccaaaacgc tgatggggag gctggaagat ggcagccccc ggactgggca gatcttcaag 1020
 cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac 1080
 gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacgtg 1140
 cagtgccgct ctgtggaggg cagctgtggc ttctcatggg gtgggtggagg aagtttccca 1200
 accattccct tatccaggct ttttgacaac gctatgctcc gcgcccacg tctgcaccag 1260
 ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat 1320
 tcattcctgc agaaccacca gacctccctc tgtttctcag agtctattcc gacacctcc 1380
 aacagggagg aaacacaaca gaaatccaac cttagagctgc tccgcatctc cctgctgctc 1440
 atccagtcgt ggctggagcc cgtgcagttc cttagagtg tcttcgcaa cagcctggg 1500
 tacggcgct ctgacagcaa cgtctatgac ctctaaagg acctagagga aggcattcaa 1560
 acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc 1620
 tacagcaagt tcgacacaaa ctacacaaac gatgacgcac tactcaagaa ctacgggctg 1680
 ctctactgct tcaggaagga catggacaag gtcgagacat tcctgcgcat cgtgcagtgc 1740
 cgctctgtgg agggcagctg tggtttctca tgaggatcc 1779

<210> 53
 <211> 589
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic sequence

<220>
 <221> MISC_FEATURE
 <222> (391)..(588)
 <223> sequence is repeated N-1 times, where N is a positive whole numbe

<220>
 <221> mat_peptide
 <222> (1)..()

<400> 53

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190
 Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu
 195 200 205
 Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe
 210 215 220
 Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys
 225 230 235 240
 Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser
 245 250 255
 Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu
 260 265 270
 Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro
 275 280 285
 Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
 290 295 300
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile
 305 310 315 320

Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln
325 330 335

Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp
340 345 350

Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp
355 360 365

Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val
370 375 380

Glu Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr
385 390 395 400

Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg
405 410 415

Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr
420 425 430

Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser
435 440 445

Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
450 455 460

Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile
465 470 475 480

Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn
485 490 495

Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys
500 505 510

Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly
515 520 525

Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp
530 535 540

Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu
545 550 555 560

Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
565 570 575

Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser
580 585

<210> 54
<211> 2370
<212> DNA
<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc_feature

<222> (1174)..(1767)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 54

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gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt	180
ccgacaccct ccaacagggg ggaacacaaa cagaaatcca acctagagct gctccgcatc	240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tctcaggag tgtcttcgcc	300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catgggggtg tggaggaagt	600
ttcccaacca ttcccttacc caggcttttt gacaacgcta tgctccgcgc ccacgtctctg	660
caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag	720
aagtattcat tctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca	780
ccctccaaca gggaggaaaac acaacagaaa tccaacctag agctgctccg catctccctg	840
ctgctcatcc agtcgtggct ggagcccgtg cagttcctca ggagtgtctt cgccaacagc	900
ctggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc	960
atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag	1020
cagacctaca gcaagttcga caaaaactca cacaacgatg acgcactact caagaactac	1080
gggctgctct actgcttcag gaaggacatg gacaaggctc agacattcct gcgcatcgtg	1140
cagtgcgcgt ctgtggaggg cagctgtggc ttctcatggg gtggtggagg aagtttccca	1200
accattccct tatccaggct ttttgacaac gctatgctcc gcgcccatcg tctgcaccag	1260
ctggcctttg acacctacca ggagtttgaa gaagcctata tcccaaagga acagaagtat	1320
tcattcctgc agaaccceca gacctccctc tgtttctcag agtctattcc gacacctcc	1380
aacagggagg aaacacaaca gaaatccaac ctagagctgc tccgcatctc cctgctgctc	1440

atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcttcgccaa cagcctgggtg 1500
 tacggcgcct ctgacagcaa cgtctatgac ctccataagg acctagagga aggcattccaa 1560
 acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc 1620
 tacagcaagt tcgacacaaa ctcacacaac gatgacgcac tactcaagaa ctacgggctg 1680
 ctctactgct tcaggaagga catggacaag gtcgagacat tcttgcgcat cgtgcagtgc 1740
 cgctctgtgg agggcagctg tggcttctca tgggggtggg gaggaagttt cccaaccatt 1800
 cccttatcca ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc 1860
 tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc 1920
 ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg 1980
 gaggaacac aacagaaatc caacctagag ctgctccga tctccctgct gctcatccag 2040
 tcgtggctgg agcccgtgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc 2100
 gcctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat ccaaacgctg 2160
 atggggaggc tggaagatgg cagcccccg actgggcaga ttttcaagca gacctacagc 2220
 aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac 2280
 tgcttcagga aggacatgga caaggtcgag acattcctgc gcacgtgca gtgccgctct 2340
 gtggagggca gctgtggctt ctagggatcc 2370

<210> 55
 <211> 786
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic sequence

<220>
 <221> MISC_FEATURE
 <222> (391)..(588)

<220>
 <221> mat_peptide
 <222> (1)..()

<400> 55

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
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Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190
 Ser Trp Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu
 195 200 205
 Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe
 210 215 220
 Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys
 225 230 235 240
 Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser
 245 250 255
 Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu
 260 265 270
 Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro
 275 280 285
 Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
 290 295 300
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile
 305 310 315 320
 Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln
 325 330 335

Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp		
			340					345					350				
Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp		
		355					360					365					
Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val		
		370				375					380						
Glu	Gly	Ser	Cys	Gly	Phe	Ser	Trp	Gly	Gly	Gly	Gly	Ser	Phe	Pro	Thr		
385					390					395					400		
Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg		
			405					410						415			
Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr		
		420						425					430				
Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser		
		435					440					445					
Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr		
	450					455					460						
Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile		
465					470				475						480		
Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn		
			485					490						495			
Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys		
		500					505						510				
Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly		
	515						520					525					
Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp		
	530					535					540						
Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu		
545				550						555					560		
Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile		
			565						570					575			
Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	Ser	Trp	Gly	Gly		
		580						585					590				
Gly	Gly	Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala		
	595						600					605					
Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln		
	610					615					620						
Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu		
625				630					635						640		

Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro
645 650 655

Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg
660 665 670

Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu
675 680 685

Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn
690 695 700

Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met
705 710 715 720

Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln
725 730 735

Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu
740 745 750

Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val
755 760 765

Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys
770 775 780

Gly Phe
785

<210> 56
<211> 33
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 56
ttaccatgga ttgccggcgg cggcggatcc aat

33

<210> 57
<211> 36
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 57
ttaccatgga tttgatcagg cggcggcgga tccaat

36

<210> 58
<211> 36

<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 58
tgatcaggcg gcggcgatc aggcggcggc ggatcc

36

<210> 59
<211> 10
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 59

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10

<210> 60
<211> 48
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 60
gcggcgccgc gcggatcagg cggcgccgga tcaggcgccg gcggatcc

48

<210> 61
<211> 14
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 61

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10

<210> 62
<211> 43
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 62

ggacatatgc tgtgatcatt cccaaccatt cccttatcca ggc

43

<210> 63

<211> 41

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 63

cgcgattcg atccatggaa gccacagctg ccctccacag a

41

<210> 64

<211> 36

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 64

cgcgctcgacc tagaagccac agctgccctc cacaga

36

<210> 65

<211> 602

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 65

catatgctgt gatcattccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60

cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 120

atcccaaagg aacagaagta ttcattctctg cagaaccccc agacctccct ctgtttctca 180

gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg 240

ctccgcatct ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 300

gtcttcgcca acagcctggg gtacggcgcc tctgacagca acgtctatga cctcctaaag 360

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420

gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480

ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540

ttcctgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttcca tggatcgaat 600

tc 602

<210> 66
<211> 192
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 66

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

<210> 67
<211> 600
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 67

catatgctgt gatcattccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60
cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 120
atcccaaagg aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca 180
gagtctattc cgacaccctc caacagggag gaaacacaa agaatccaa cctagagctg 240
ctccgcatct cctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 300
gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 360
gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420
gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480
ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540
ttcctgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttcta ggtcgacgcg 600

<210> 68
<211> 192
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 68

Ser	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu
1				5					10					15	
Arg	Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe
		20						25					30		
Glu	Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn
		35					40					45			
Pro	Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn
		50				55					60				
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser
65				70						75				80	
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser
			85						90					95	
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
		100						105					110		
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg
		115				120						125			
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr
	130					135						140			

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

<210> 69
 <211> 639
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 69
 catatgctgt gatcattccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 60
 cgcgcccatc gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat 120
 atcccaaagg aacagaagta ttcatctctg cagaaccccc agacctccct ctgtttctca 180
 gagtctattc cgacacctc caacagggag gaaacacaa agaaatccaa cctagagctg 240
 ctccgcatct cctgctgct catccagtcg tggctggagc cegtgcagtt cctcaggagt 300
 gtcttcgcca acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 360
 gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag cccccggact 420
 gggcagatct tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca 480
 ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540
 ttctgcgca tegtgcagtg ccgtctgtg gagggcagct gtggcttcgg cggcggcgga 600
 tcaggcggcg gcggatcagg cggcggcgga tccgaattc 639

<210> 70
 <211> 206
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 70

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 195 200 205

<210> 71
 <211> 630
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 71
 catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccatt 60
 cgtctgcacc agctggcctt tgacaccta caggagtttg aagaagccta taccctaaag 120
 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180
 ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240
 tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc 300
 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360
 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg gcggcggcgg atcaggcggc 600
ggcggatcag gcggcggcgg atccgaattc 630

<210> 72
<211> 206
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 72

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15
Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30
Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45
Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60
Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80
Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95
Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110
Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125
Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160
Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175
Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
195 200 205

<210> 73
<211> 1248
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<220>
<221> misc_feature
<222> (619)..(1236)
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 73
tgatcattcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60
cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gtcgcgcac 240
tccctgctgc tcattccagtc gtggctggag ccgctgcagt tcctcaggag tgtcttcgcc 300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg gcggcggcgg atcaggcggc 600
ggcggatcag gcggcggcgg atcattccca accattccct tatccaggct ttttgacaac 660
gctatgctcc gcgcccacg tctgcaccag ctggcctttg acacctacca ggagtttgaa 720
gaagcctata tcccaaagga acagaagtat tcattcctgc agaacccccca gacctccctc 780
tgtttctcag agtctattcc gacacctcc aacagggagg aaacacaaca gaaatccaac 840
ctagagctgc tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagttc 900
ctcaggagtg tcttcgcaa cagcctggtg tacggcgct ctgacagcaa cgtctatgac 960
ctcctaaagg acctagagga aggcattcaa acgctgatgg ggaggctgga agatggcagc 1020
ccccggactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctacacaaac 1080
gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag 1140
gtcgagacat tcctgcgcac cgtgcagtgc cgctctgtgg agggcagctg tggcttcggc 1200

<210> 74

<211> 412

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC_FEATURE

<222> (193)..(398)

<223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 74

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe

195	200	205
Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala 210 215 220		
His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu 225 230 235 240		
Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln 245 250 255		
Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu 260 265 270		
Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu 275 280 285		
Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe 290 295 300		
Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu 305 310 315 320		
Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu 325 330 335		
Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys 340 345 350		
Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly 355 360 365		
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu 370 375 380		
Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly 385 390 395 400		
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly 405 410		

<210> 75
 <211> 2445
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<220>
 <221> misc_feature
 <222> (1237)..(1854)
 <223> sequence is repeated N-1 times, where N is a positive whole numbe

<400> 75

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gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt	180
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac	240
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc	300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc	420
ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttgc gcggcgccgg atcaggcggc	600
ggcggatcag gcggcgccgg atcattccca accattccct tatccaggct ttttgacaac	660
gctatgctcc gcgcccacgc tctgcaccag ctggcctttg acacctacca ggagtttgaa	720
gaagcctata tcccaaagga acagaagtat tcatctctgc agaaccacca gacctccctc	780
tgttttctcag agtctattcc gacacctcc aacagggagg aaacacaaca gaaatccaac	840
ctagagctgc tccgcatctc cctgctgctc atccagtcgt ggctggagcc cgtgcagtcc	900
ctcaggagtg tcttcgcca cagcctggtg tacggcgccct ctgacagcaa cgtctatgac	960
ctcctaaagg acctagagga aggcattccaa acgctgatgg ggaggctgga agatggcagc	1020
ccccggactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctcacacaac	1080
gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag	1140
gtcgagacat tcttgccat cgtgcagtgc cgctctgtgg agggcagctg tggcttcggc	1200
ggcggcggat caggcggcgg cggatcaggc ggcggcggat cattcccaac cattccctta	1260
tccaggcttt ttgacaacgc tatgctccgc gccatcgctc tgcaccagct ggcctttgac	1320
acctaccagg agtttgaaga agcctatatc ccaaagggaac agaagtattc attcctgcag	1380
aacccccaga cctccctctg tttctcagag tctattccga cacctccaa caggaggaa	1440
acacaacaga aatccaacct agagctgctc cgcattctcc tgctgctcat ccagtcgtgg	1500
ctggagcccc tgcagttcct caggagtgtc ttgcgcaaca gcctggtgta cggcgccctc	1560
gacagcaacg tctatgacct cctaaaggac ctagaggaag gcatccaaac gctgatgggg	1620
aggctggaag atggcagccc ccggactggg cagatcttca agcagacctc cagcaagtcc	1680
gacacaaact cacacaacga tgacgcacta ctcaagaact acgggctgct ctactgcttc	1740

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aggaaggaca tggacaaggt cgagacattc ctgcgcatcg tgcagtgccg ctctgtggag 1800
ggcagctgtg gcttcggcgg cggcggatca ggcggcggcg gatcaggcgg cggcggatca 1860
ttcccaacca ttcccttata caggtttttt gacaacgcta tgctccgcgc ccatcgtctg 1920
caccagctgg cctttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 1980
aagtattcat tctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca 2040
ccctccaaca gggaggaaac acaacagaaa tccaacctag agctgctccg catctccctg 2100
ctgctcatcc agtcgtggct ggagcccggt cagttcctca ggagtgtctt cgccaacagc 2160
ctggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc 2220
atccaaacgc tgatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag 2280
cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac 2340
gggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcatcgtg 2400
cagtgccgct ctgtggaggg cagctgtggc ttctaggtcg acgcg 2445

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<210> 76
<211> 810
<212> PRT
<213> Artificial

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<220>
<223> synthetic sequence

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<220>
<221> MISC_FEATURE
<222> (412)..(617)
<223> sequence is repeated N-1 times, where N is a positive whole numbe

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<220>
<221> mat_peptide
<222> (1)..()

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<400> 76

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Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1           5           10          15

```

```

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
          20           25           30

```

```

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
          35           40           45

```

```

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn

```

50					55					60					
Arg	Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser
65					70					75					80
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser
			85						90					95	
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
			100					105					110		
Asp	Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg
			115				120					125			
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr
			130				135					140			
Ser	Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn
145					150					155				160	
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr
				165					170					175	
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe
			180					185					190		
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Phe
			195				200					205			
Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala
			210				215					220			
His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu
225					230					235				240	
Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln
				245					250					255	
Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu
			260					265					270		
Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu
			275				280					285			
Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe
			290				295					300			
Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu
305					310					315				320	
Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu
				325					330					335	
Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys
			340					345					350		
Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly

355	360	365
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu		
370	375	380
Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly		
385	390	395 400
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Phe Pro Thr		
	405 410	415
Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg		
	420 425	430
Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr		
	435 440	445
Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser		
	450 455	460
Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr		
465	470 475	480
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile		
	485 490	495
Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn		
	500 505	510
Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys		
	515 520	525
Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly		
	530 535	540
Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp		
545	550 555	560
Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu		
	565 570	575
Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile		
	580 585	590
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly Gly		
	595 600	605
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Pro Thr Ile Pro		
	610 615	620
Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His		
625	630 635	640
Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro		
	645 650	655
Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys		

660					665					670									
Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln				
675					680					685									
Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser				
690					695					700									
Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu				
705					710					715					720				
Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu				
725					730					735									
Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro				
740					745					750									
Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn				
755					760					765									
Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys				
770					775					780									
Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln				
785					790					795					800				
Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe										
805					810														

<210> 77
 <211> 593
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<400> 77
 catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60
 cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120
 gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180
 ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240
 tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc 300
 aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360
 gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420
 ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480
 aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540
 atcgtgcagt gccgctctgt ggagggcagc tgtggcttcc atggatcgaa ttc 593

<210> 78
<211> 192
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 78

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

<210> 79
<211> 592
<212> DNA
<213> Artificial

<220>
<223> synthetic sequence

<400> 79

aagctttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc cgcgcccac 60
gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg 120
aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc 180
cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg ctccgcatct 240
ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca 300
acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg 360
aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccgaggact gggcagatct 420
tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga 480
actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttctgcgca 540
tcgtgcagtg ccgctctgtg gagggcagct gtggcttcca tggatcgaat tc 592

<210> 80
<211> 191
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<400> 80

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
1 5 10 15

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
35 40 45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
50 55 60

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
85 90 95

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
 145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
 165 170 175

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

<210> 81

<211> 587

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 81

aagctttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc cgcgcccac 60

gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg 120

aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc 180

cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg ctccgcatct 240

cctgtctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca 300

acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg 360

aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccgaggact gggcagatct 420

tcaagcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga 480

actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttcttgcgca 540

tcgtgcagtg ccgctctgtg gagggcagct gtggcttcta gggatcc 587

<210> 82

<211> 191

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<400> 82

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
 1 5 10 15

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
 20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro

35					40					45					
Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg
50						55					60				
Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu
65					70				75					80	
Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val
				85				90						95	
Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp
		100						105					110		
Leu	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu
		115					120					125			
Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser
	130					135					140				
Lys	Phe	Asp	Thr	Asn	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr
145				150						155				160	
Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe
			165					170					175		
Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	
		180						185					190		

<210> 83
 <211> 1165
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence

<220>
 <221> misc_feature
 <222> (579)..(1151)
 <223> sequence is repeated N-1 times, where N is a positive whole number

<400> 83
 aagctttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc cgcgcccac 160
 gtctgcacca gctggccttt gacacctacc aggagtttga agaagcctat atcccaaagg 120
 aacagaagta ttcattcctg cagaaccccc agacctccct ctgtttctca gagtctattc 180
 cgacaccctc caacaggag gaaacacaac agaaatccaa cctagagctg ctccgcatct 240
 ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca 300
 acagcctggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg 360

aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccggaact gggcagatct 420
tcaagcagac ctacagcaag ttcgacacaa actcacaçaa cgatgacgca ctactcaaga 480
actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttcctgcgca 540
tcgtgcagtg ccgctctgtg gagggcagct gtggcttctt cccaaccatt cccttatcca 600
ggctttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc tttgacacct 660
accaggagtt tgaagaagcc tatatcccaa aggaacagaa gtattcattc ctgcagaacc 720
cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg gaggaaacac 780
aacagaaatc caacctagag ctgctccgca tctccctgct gctcatccag tcgtggctgg 840
agcccgtgca gttcctcagg agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca 900
gcaacgtcta tgacctccta aaggacctag aggaaggcat ccaaacgctg atggggaggc 960
tggaagatgg cagcccccg actgggcaga tcttcaagca gacctacagc aagtctgaca 1020
caaactcaca caacgatgac gcactactca agaactacgg gctgctctac tgcttcagga 1080
aggacatgga caaggctgag acattcctgc gcacgtgca gtgccgctct gtggagggca 1140
gctgtggctt ccatggatcg aattc 1165

<210> 84
<211> 191
<212> PRT
<213> Artificial
<220>
<223> synthetic sequence
<220>
<221> MISC_FEATURE
<222> (1)..(191)
<223> sequence is repeated N times, where N is a positive whole number

<400> 84

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
1 5 10 15

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu
20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
35 40 45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg
50 55 60

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val
85 90 95

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu
115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser
130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr
145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe
165 170 175

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

<210> 85

<211> 2307

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc_feature

<222> (1153)..(1725)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 85

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcccac 60

cgtctgcacc agctggcctt tgacacctac caggagtttg aagaagccta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180

ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac 240

tccttgctgc tcatccagtc gtggctggag cccgtgcagt tcttcaggag tgtcttcgcc 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaagcaga cctacagcaa gtctgacaca aactcacaca acgatgacgc actactcaag 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgagc	540
atcgtgcagt gccgctctgt ggagggcagc tgtggcttct tcccaaccat tcccttatcc	600
aggctttttg acaacgctat gctccgagcc catcgtctgc accagctggc ctttgacacc	660
taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac	720
ccccagacct ccctctgttt ctacagagtct attccgacac cctccaacag ggaggaaaca	780
caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg	840
gagcccgtgc agttccctcag gagtgtcttc gccaacagcc tgggtgtacgg cgcctctgac	900
agcaacgtct atgacctcct aaaggaccta gaggaaggca tccaaacgct gatggggagg	960
ctggaagatg gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac	1020
acaaactcac acaacgatga cgcactactc aagaactacg ggctgctcta ctgcttcagg	1080
aaggacatgg acaaggtcga gacattcctg cgcacgtgc agtgccgctc tgtggagggc	1140
agctgtggct tcttcccaac cattccctta tccaggcttt ttgacaacgc tatgctccgc	1200
gcccatcgtc tgcaccagct ggcttttgac acctaccagg agtttgaaga agcctatata	1260
ccaaaggaaac agaagtattc attcctgcag aacccccaga cctccctctg tttctcagag	1320
tctattccga caccctcaa cagggaggaa acacaacaga aatccaacct agagctgctc	1380
cgcactctcc tgctgctcat ccagtcgtgg ctggagcccg tgcagttcct caggagtgtc	1440
ttcgccaaca gcctgggtga cggcgctct gacagcaacg tctatgacct cctaaaggac	1500
ctagaggaag gcatccaaac gctgatgggg aggttggaag atggcagccc ccggactggg	1560
cagatcttca agcagacct cagcaagttc gacacaaact cacacaacga tgacgcacta	1620
ctcaagaact acgggctgct ctactgcttc aggaaggaca tggacaaggc cgagacattc	1680
ctgcgcacgc tgcagtgcg ctctgtggag ggcagctgtg gcttcttccc aaccattccc	1740
ttatccaggc tttttgacaa cgctatgctc cgcgcccatc gtctgcacca gctggccttt	1800
gacacctacc aggagtttga agaagcctat atcccaaagg aacagaagta ttcattcctg	1860
cagaaccccc agacctcct ctgtttctca gagtctattc cgacaccctc caacagggag	1920
gaaacacaac agaaatcaa cctagagctg ctccgcactc cctgctgct catccagtcg	1980
tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca acagcctggt gtacggcgcc	2040
tctgacagca acgtctatga cctcctaaag gacctagagg aaggcatcca aacgctgatg	2100
gggaggctgg aagatggcag cccccggact gggcagatct tcaagcagac ctacagcaag	2160
ttcgacacaa actcacacaa cgatgacgca ctactcaaga actacgggct gctctactgc	2220

ttcaggaagg acatggacaa ggtcgagaca ttcctgcgca tcgtgcagtg ccgctctgtg 2280
gagggcagct gtggcttcta gggatcc 2307

<210> 86
<211> 192
<212> PRT
<213> Artificial

<220>
<223> synthetic sequence

<220>
<221> MISC_FEATURE
<222> (2)..(192)
<223> sequence is repeated N+2 times, where N is a positive whole numbe

<220>
<221> mat_peptide
<222> (1)..()

<400> 86

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190